Amendments to the claims

In accordance with the revised format for claim amendments, all claims are shown below. Please amend the claims as follows:

1. (Currently amended) A composition comprising a ~~substantially purified~~ thermostable GuxA peptide heterologously expressed in an organism other than *Acidothermus cellulolyticus*, said GuxA peptide comprising a first catalytic domain GH6, a second catalytic domain GH 12, a carbohydrate binding domain (CBD) type III, and a carbohydrate binding domain (CBD) type II.

2. (original) The composition of claim 1 wherein the Gux A peptide is further defined as comprising a linker and a signal peptide.

3. (Previously presented) The composition of claim 1 wherein the GH6 catalytic domain of the GuxA peptide is further defined as having a length of about 420 to about 425 amino acids.

4. (original) The composition of claim 1, 2 or 3 wherein the GH12 catalytic domain of the GuxA peptide is further defined as having a length of about 225 to about 235 amino acids.

5. (Previously presented) The composition of claim 1, 2, or 3 wherein the carbohydrate binding domain (CBD) type III of the GuxA peptide is further defined as having a length of about 145 to about 155 amino acids.

6. (Previously presented) The composition of claim 1, 2, or 3 wherein the carbohydrate binding domain (CBD) type II of the GuxA peptide is further defined as having a length of about 95 amino acids to about 105 amino acids in length.

7. (original) The composition of claim 3 wherein the GH6 catalytic domain is further defined as the sequence of SEQ ID NO: 4.

8. (original) The composition of claim 4 wherein the GH12 catalytic domain is further defined as the sequence of SEQ ID NO: 7.

9. (original) The composition of claim 5 wherein the carbohydrate binding domain (CBD) type III is further defined as the sequence of SEQ ID NO: 5.

10. (Previously presented) The composition of claim 6 wherein the carbohydrate binding domain (CBD) type II is further defined as the sequence of SEQ ID NO:8.

11. (original) The composition of claim 1 further defined as comprising a sequence of SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 5 and SEQ ID NO: 8.

12. (original) A thermal tolerant GuxA peptide having a sequence of SEQ ID NO: 1.

13. (Previously presented) The GuxA peptide of claim 12 further defined as having a sequence encoded by SEQ ID NO: 2.

14. (original) An industrial mixture suitable for degrading cellulose, such mixture comprising the GuxA polypeptide of claim 1.

15. (original) The industrial mixture of claim 14 further defined as comprising a detergent.

16. (Previously presented) The composition of claim 1 wherein the GuxA peptide is further defined as comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4.

17. (Previously presented) The composition of claim 1 wherein the GuxA peptide is further defined as comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7.

18. (Previously presented) The composition of claim 1 wherein the GuxA peptide is further defined as comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5.

19. (Previously presented) The composition of claim 1 wherein the GuxA peptide is further defined as comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8.

20. (Previously presented) The composition of claim 1 wherein the GuxA peptide is further defined as comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1.

21. (Previously presented) The composition of claim 1 wherein the GuxA peptide is further defined as comprising an amino acid sequence encoded by a nucleic acid sequence having at least 90% identity to SEQ ID NO: 2.

22. (Currently amended) The composition of claim 1 ~~wherein the GuxA peptide is further defined as comprising a heterologous combination of the first catalytic domain GH6, the second catalytic domain GH 12, the carbohydrate binding domain (CBD) type III, and the carbohydrate binding domain (CBD) type II~~ further comprising a heterologous peptide fused with said GuxA peptide.

23. (Currently amended) The composition of claim 22 wherein the heterologous ~~combination~~ peptide comprises a peptide tag.

24. (Previously presented) The composition of claim 23 wherein the peptide tag is 6-His, thioredoxin, hemaglutinin, GST, or OmpA signal sequence tag.

24-26. (Previously cancelled)

27. (Currently amended) An isolated polypeptide molecule comprising:
a) a sequence of SEQ ID NO: 4;
b) a sequence of SEQ ID NO: 7;
c) a sequence of SEQ ID NO: 5;
d) a sequence of SEQ ID NO: 8;
e) a sequence of SEQ ID NO: 1; or
f) an amino acid sequence having at least 70% sequence identity with the amino acid sequence of a), b), c), d), or e) and having ~~a functionality of~~ at least one domain of glycosyl hydrolase family 6 and glycosyl hydrolase family 12.

28. (original) The polypeptide molecule of claim 27, having at least 90% sequence identity with the amino acid sequence of a), b), c), d), or e).

29. (original) A fusion protein comprising the polypeptide of claim 14 and a heterologous peptide.

30. (original) The fusion protein of claim 29, wherein the heterologous peptide is a substrate targeting moiety.

31. (original) The fusion protein of claim 29, wherein the heterologous peptide is a peptide tag.

32. (original) The fusion protein of claim 31, wherein the peptide tag is 6- His, thioredoxin, hemaglutinin, GST, or OmpA signal sequence tag.

33. (original) The fusion protein of claim 29, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

34. (original) The fusion protein of claim 29, wherein the agent is a leucine zipper.

35. (original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 27 bound to cellulose.

36-42. (Previously cancelled)

43. (original) A composition comprising the polypeptide molecule of claim 27 and a carrier.

44. (original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

45-47. (Previously cancelled)

48. (Previously presented) A method for producing GuxA polypeptide, the method comprising:
incubating a host cell genetically engineered to express the polypeptide molecule of claim 27.

49. (Previously presented) The method of claim 48, further comprising the step of: isolating the polypeptide molecule from the incubated host cell.

50. (original) The method of claim 49, wherein the host cell is a plant cell.

51. (original) The method of claim 49, wherein the host cell is a bacterial cell.

52. (original) The method of claim 49, wherein the host cell is genetically engineered to express a selectable marker.

53. (original) The method of claim 49, wherein the host cell further comprises a polynucleotide molecule encoding one or more polypeptide molecules selected from the glycoside hydrolase family of proteins.

54. (Previously presented) The method of claim 53, wherein the glycoside hydrolase is a thermostable glycoside hydrolase.

55-57. (Previously cancelled)

58. (Previously presented) A method for assessing the carbohydrate hydrolysis activity of GuxA comprising: analyzing a carbohydrate hydrolysis in the presence of GuxA and a carbohydrate
hydrolysis in the absence of GuxA on a substrate; and comparing the carbohydrate hydrolysis in the presence of GuxA with the carbohydrate hydrolysis in the absence of GuxA.

59. (Previously presented) A method for assessing the carbohydrate hydrolysis activity of GuxA in the presence of an agent of interest comprising:

analyzing a carbohydrate hydrolysis in the presence of GuxA and a carbohydrate hydrolysis in the presence of GuxA and the agent of interest on a substrate; and comparing the carbohydrate hydrolysis in the GuxA treated substrate with the carbohydrate hydrolysis in the GuxA treated substrate in the presence of the agent of interest.

60. (Previously presented) The method of claim 59, wherein an increase in carbohydrate hydrolysis activity in the presence of the agent of interest demonstrates stimulation of GuxA activity and wherein a decrease in carbohydrate hydrolysis activity demonstrates inhibition of GuxA activity.

61. (original) The method of claim 58, wherein the carbohydrate is cellulose.

62. (Previously presented) The method of claim 59 wherein the agent of interest is an antibody.

63. (Previously presented) A method for hydrolyzing cellulose in a starting material, the method comprising:
administering to the starting material an effective amount of a polypeptide molecule of claim 27.

64. (Previously presented) The method of claim 63, further comprising administering a second polypeptide molecule selected from the glycoside hydrolase family of proteins.

65. (original) The method of claim 63, wherein the polypeptide molecule of claim 27 is thermostable.

66. (original) The method of claim 63, wherein the starting material is agricultural biomass.

67. (original) The method of claim 63, wherein the starting material is municipal solid waste.

68. (Currently amended) The composition of claim 22 wherein the heterologous ~~combination~~ peptide further comprises a substrate targeting moiety.

69. (New) A composition comprising a GuxA-derived peptide, said peptide comprising at least one catalytic domain selected from GH6 and GH 12 domains, and at least one carbohydrate binding domain selected from CBD type II and CBD type III domains.

70. (New) The composition of claim 69 further comprising a heterologous peptide fused with said GuxA-derived peptide.

71. (New) The fusion protein of claim 70 wherein said heterologous peptide is a peptide tag.

72. (New) The fusion protein of claim 70 wherein said heterologous peptide comprises a catalytic domain of a glycoside hydrolase other than GuxA.

73. (New) The fusion protein of claim 70 wherein said heterologous peptide comprises a binding domain of a glycoside hydrolase other than GuxA.

74. (New) The composition of claim 2, wherein the signal peptide is at least 60 percent identical to SEQ ID No. 3.

75. (New) The composition of claim 2, wherein the signal peptide is derived from the signal peptide of other secretory proteins.